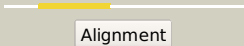
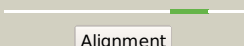

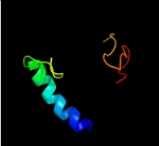
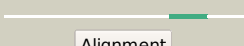





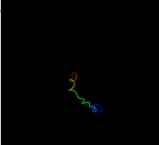

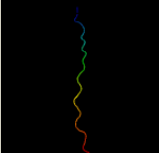
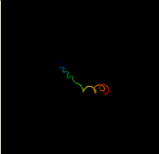
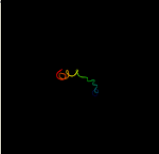
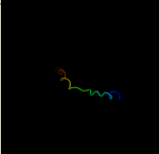
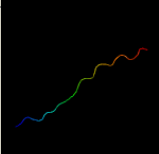
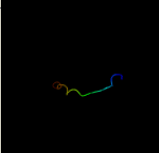
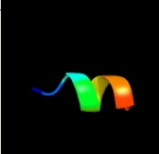



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2183c_(-)_2445423_2445818
Date	Mon Aug 5 13:25:30 BST 2019
Unique Job ID	efe1e92cd725b08a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4mb7A_</a>	 Alignment		70.7	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease 8-like I720; <b>PDBTitle:</b> crystal structure of a viral dna glycosylase
2	<a href="#">c3a1hF_</a>	 Alignment		54.9	45	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
3	<a href="#">c3twkB_</a>	 Alignment		52.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formamidopyrimidine-dna glycosylase 1; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana fpg
4	<a href="#">c3a0aC_</a>	 Alignment		50.6	43	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
5	<a href="#">c2opfA_</a>	 Alignment		48.2	29	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease viii; <b>PDBTitle:</b> crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
6	<a href="#">c3a1hA_</a>	 Alignment		45.5	41	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
7	<a href="#">d1woua_</a>	 Alignment		44.6	45	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> TxnI5-like
8	<a href="#">c3a1hE_</a>	 Alignment		44.2	39	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
9	<a href="#">c3a1hD_</a>	 Alignment		44.2	39	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
10	<a href="#">c3a1hC_</a>	 Alignment		44.2	39	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
11	<a href="#">c1x1kD_</a>	 Alignment		43.0	42	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4

12	<a href="#">c1x1kC</a>	Alignment		43.0	42	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-pro-gly)4 <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-pro-gly)4
13	<a href="#">c2d3fF</a>	Alignment		43.0	42	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp-gly-(pro-pro-gly)4 <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
14	<a href="#">c1x1kA</a>	Alignment		43.0	42	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-pro-gly)4 <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-pro-gly)4
15	<a href="#">c2d3fD</a>	Alignment		43.0	42	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp-gly-(pro-pro-gly)4 <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
16	<a href="#">c2d3fE</a>	Alignment		43.0	42	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp-gly-(pro-pro-gly)4 <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
17	<a href="#">c1x1kB</a>	Alignment		43.0	42	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-pro-gly)4 <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-pro-gly)4
18	<a href="#">c3a0aA</a>	Alignment		41.6	41	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
19	<a href="#">d1wjka</a>	Alignment		40.9	56	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
20	<a href="#">c1k82D</a>	Alignment		40.9	24	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> D: <b>PDB Molecule:</b> formamidopyrimidine-dna glycosylase; <b>PDBTitle:</b> crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
21	<a href="#">d2hyja2</a>	Alignment	not modelled	40.9	18	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
22	<a href="#">d1v9wa</a>	Alignment	not modelled	40.7	42	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> TxnI5-like
23	<a href="#">c3a0aF</a>	Alignment	not modelled	39.7	43	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
24	<a href="#">c3a1hB</a>	Alignment	not modelled	38.2	41	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
25	<a href="#">c3a0aE</a>	Alignment	not modelled	37.2	43	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
26	<a href="#">c3a0aB</a>	Alignment	not modelled	36.8	43	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
27	<a href="#">c2vvyC</a>	Alignment	not modelled	36.2	42	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> protein b15; <b>PDBTitle:</b> structure of vaccinia virus protein b14
28	<a href="#">c3abnC</a>	Alignment	not modelled	35.7	43	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 a
29	<a href="#">c3admC</a>	Alignment	not modelled	35.1	42	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4

						gly)4
30	<a href="#">c3a0mC_</a>	Alignment	not modelled	34.9	42	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
31	<a href="#">c3a0mB_</a>	Alignment	not modelled	34.6	43	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
32	<a href="#">c3w0fA_</a>	Alignment	not modelled	33.6	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease 8-like 3; <b>PDBTitle:</b> crystal structure of mouse endonuclease viii-like 3 (mnei3)
33	<a href="#">c2d3fC_</a>	Alignment	not modelled	32.4	39	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
34	<a href="#">c2d3fB_</a>	Alignment	not modelled	32.4	39	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
35	<a href="#">c1x1kE_</a>	Alignment	not modelled	32.4	39	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
36	<a href="#">c2d3fA_</a>	Alignment	not modelled	32.4	39	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
37	<a href="#">c3admE_</a>	Alignment	not modelled	30.9	42	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
38	<a href="#">c3admB_</a>	Alignment	not modelled	30.9	42	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
39	<a href="#">c3admA_</a>	Alignment	not modelled	30.9	42	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
40	<a href="#">c3admF_</a>	Alignment	not modelled	30.9	42	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
41	<a href="#">c2qsiB_</a>	Alignment	not modelled	27.6	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative hydrogenase expression/formation protein hupg; <b>PDBTitle:</b> crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodospseudomonas palustris cga009
42	<a href="#">c3abnA_</a>	Alignment	not modelled	26.9	42	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 a
43	<a href="#">c4fybA_</a>	Alignment	not modelled	26.7	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein (dsbc); <b>PDBTitle:</b> structural and functional characterizations of a thioredoxin-fold2 protein from helicobacter pylori
44	<a href="#">d1z6na1</a>	Alignment	not modelled	26.6	67	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
45	<a href="#">c2he3A_</a>	Alignment	not modelled	25.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione peroxidase 2; <b>PDBTitle:</b> crystal structure of the selenocysteine to cysteine mutant of human2 glutathione peroxidase 2 (gpx2)
46	<a href="#">c5a4hA_</a>	Alignment	not modelled	25.4	39	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-acylglycerol-3-phosphate o-acyltransferase abhd5; <b>PDBTitle:</b> solution structure of the lipid droplet anchoring peptide2 of cgi-58 bound to dpc micelles
47	<a href="#">c3a0aD_</a>	Alignment	not modelled	25.3	47	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
48	<a href="#">d1knga_</a>	Alignment	not modelled	25.2	43	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
49	<a href="#">c4tr3A_</a>	Alignment	not modelled	25.1	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> type iii iodothyronine deiodinase; <b>PDBTitle:</b> mouse iodothyronine deiodinase 3 catalytic core, semet-labeled active2 site mutant secys->cys
50	<a href="#">d1z5ye1</a>	Alignment	not modelled	24.8	50	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
51	<a href="#">c3a46B_</a>	Alignment	not modelled	24.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formamidopyrimidine-dna glycosylase; <b>PDBTitle:</b> crystal structure of mvnei1/thf complex
52	<a href="#">c1cagA_</a>	Alignment	not modelled	23.3	32	<b>PDB header:</b> collagen <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution
53	<a href="#">c1cagC_</a>	Alignment	not modelled	23.3	32	<b>PDB header:</b> collagen <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution

54	<a href="#">c5mpeZ</a>	Alignment	not modelled	22.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> Z: <b>PDB Molecule:</b> 26s proteasome regulatory subunit rp1; <b>PDBTitle:</b> 26s proteasome in presence of atp (s2)
55	<a href="#">c1cagB</a>	Alignment	not modelled	22.7	35	<b>PDB header:</b> collagen <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution
56	<a href="#">c1cgdA</a>	Alignment	not modelled	22.7	35	<b>PDB header:</b> collagen <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> hydration structure of a collagen peptide
57	<a href="#">c1cgdC</a>	Alignment	not modelled	22.7	35	<b>PDB header:</b> collagen <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> hydration structure of a collagen peptide
58	<a href="#">c1cgdB</a>	Alignment	not modelled	22.7	35	<b>PDB header:</b> collagen <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> hydration structure of a collagen peptide
59	<a href="#">c3a0mD</a>	Alignment	not modelled	22.0	39	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
60	<a href="#">d1sgma2</a>	Alignment	not modelled	22.0	22	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
61	<a href="#">c2fgxA</a>	Alignment	not modelled	21.7	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioredoxin; <b>PDBTitle:</b> solution nmr structure of protein ne2328 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net3.
62	<a href="#">c1v98A</a>	Alignment	not modelled	20.2	60	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure analysis of thioredoxin from thermus thermophilus
63	<a href="#">d1o73a</a>	Alignment	not modelled	20.0	57	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
64	<a href="#">d2fy6a1</a>	Alignment	not modelled	19.5	83	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
65	<a href="#">c3abnB</a>	Alignment	not modelled	19.2	39	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 a
66	<a href="#">c2yzhD</a>	Alignment	not modelled	19.1	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> probable thiol peroxidase; <b>PDBTitle:</b> crystal structure of peroxiredoxin-like protein from aquifex aeolicus
67	<a href="#">c3s9fA</a>	Alignment	not modelled	19.0	67	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> tryparedoxin; <b>PDBTitle:</b> the structure of tryparedoxin i from leishmania major
68	<a href="#">c3admD</a>	Alignment	not modelled	18.6	39	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
69	<a href="#">d1qgva</a>	Alignment	not modelled	18.3	33	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> spliceosomal protein U5-15Kd
70	<a href="#">d2fwha1</a>	Alignment	not modelled	18.1	60	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
71	<a href="#">c2lrcA</a>	Alignment	not modelled	18.1	44	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable thioredoxin; <b>PDBTitle:</b> structure of thioredoxin 2 from pseudomonas aeruginosa pao1 in its2 reduced form
72	<a href="#">c4m90A</a>	Alignment	not modelled	17.8	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tumor suppressor candidate 3; <b>PDBTitle:</b> crystal structure of oxidized hn33/tusc3
73	<a href="#">d1j08a1</a>	Alignment	not modelled	17.6	22	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
74	<a href="#">c3f9uA</a>	Alignment	not modelled	17.5	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported cytochrome c biogenesis-related protein; <b>PDBTitle:</b> crystal structure of c-terminal domain of putative exported cytochrome2 c biogenesis-related protein from bacteroides fragilis
75	<a href="#">c6gn9A</a>	Alignment	not modelled	17.4	60	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of a thioredoxin from clostridium acetobutylicum at2 1.75 a resolution
76	<a href="#">c2b1kA</a>	Alignment	not modelled	17.3	57	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbe; <b>PDBTitle:</b> crystal structure of e. coli ccmg protein
77	<a href="#">c1qsuB</a>	Alignment	not modelled	17.1	24	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein ((pro-hyp-gly)4- glu-lys-gly(pro-hyp-gly)5); <b>PDBTitle:</b> crystal structure of the triple-helical collagen-like peptide, (pro-2 hyp-gly)4-glu-lys-gly(pro-hyp-gly)5
78	<a href="#">c1qsuA</a>	Alignment	not modelled	17.1	24	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein ((pro-hyp-gly)4- glu-lys-gly(pro-hyp-gly)5); <b>PDBTitle:</b> crystal structure of the triple-helical collagen-like peptide, (pro-2 hyp-gly)4-glu-lys-gly(pro-hyp-gly)5
79	<a href="#">c2v2aC</a>	Alignment	not modelled	17.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> peroxiredoxin 6;

79	<a href="#">c2vzgc</a>	Alignment	not modelled	17.0	20	<b>PDBTitle:</b> crystal structure of the c45s mutant of the peroxiredoxin 62 of arenicola marina. monoclinic form
80	<a href="#">c3a0mE</a>	Alignment	not modelled	16.7	41	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
81	<a href="#">c4euyA</a>	Alignment	not modelled	16.7	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of thioredoxin-like protein bce_0499 from bacillus2 cereus atcc 10987
82	<a href="#">d2f8aa1</a>	Alignment	not modelled	16.6	0	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
83	<a href="#">d2nysa1</a>	Alignment	not modelled	16.4	26	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> AGR C 3712p-like
84	<a href="#">c2nysA</a>	Alignment	not modelled	16.4	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> agr_c_3712p; <b>PDBTitle:</b> x-ray crystal structure of protein agr_c_3712 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr88.
85	<a href="#">d1dbya</a>	Alignment	not modelled	16.4	44	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
86	<a href="#">c1x1kF</a>	Alignment	not modelled	16.2	36	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
87	<a href="#">c5ganD</a>	Alignment	not modelled	15.9	20	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> spliceosomal protein dib1; <b>PDBTitle:</b> the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom
88	<a href="#">d2b5xa1</a>	Alignment	not modelled	15.9	43	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
89	<a href="#">c2rupA</a>	Alignment	not modelled	15.8	53	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> p2x purinoceptor 4; <b>PDBTitle:</b> solution structure of rat p2x4 receptor head domain
90	<a href="#">c3w6gP</a>	Alignment	not modelled	15.6	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> P: <b>PDB Molecule:</b> probable peroxiredoxin; <b>PDBTitle:</b> structure of peroxiredoxin from anaerobic hyperthermophilic archaeon2 pyrococcus horikoshii
91	<a href="#">d1j08a2</a>	Alignment	not modelled	15.5	60	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
92	<a href="#">c3raza</a>	Alignment	not modelled	15.5	43	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-related protein; <b>PDBTitle:</b> the crystal structure of thioredoxin-related protein from neisseria2 meningitidis serogroup b
93	<a href="#">d2fiya1</a>	Alignment	not modelled	15.3	30	<b>Fold:</b> FdhE-like <b>Superfamily:</b> FdhE-like <b>Family:</b> FdhE-like
94	<a href="#">c3ah9E</a>	Alignment	not modelled	15.2	28	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
95	<a href="#">c3ah9B</a>	Alignment	not modelled	15.2	28	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
96	<a href="#">c3ah9C</a>	Alignment	not modelled	15.2	28	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
97	<a href="#">d1zmaa1</a>	Alignment	not modelled	15.2	60	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
98	<a href="#">c3nznA</a>	Alignment	not modelled	15.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> the crystal structure of the glutaredoxin from methanosarcina mazei2 go1
99	<a href="#">c2ywiA</a>	Alignment	not modelled	15.1	40	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical conserved protein; <b>PDBTitle:</b> crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus